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        RAW SEQUENCE LISTING            DATE: 08/01/2000
        PATENT APPLICATION:  US/09/367,013A    TIME: 16:10:58

        Input Set : A:\Cgabl.app
        Output Set: N:\CRF3\08012000\I367013A.raw

 3 <110> APPLICANT: KNUTZON, DEBORAH
 4         MUKERJI, PRADIP
 5         HUANG, YUNG-SHENG
 6         THURMOND, JENNIFER
 7         CHAUDHARY, SUNITA
 8         LEONARD, AMANDA E.
10 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS OF LONG CHAIN
11         POLYUNSATURATED FATTY ACIDS
13 <130> FILE REFERENCE: CGAB-210 USA
15 <140> CURRENT APPLICATION NUMBER: 09/367,013A
16 <141> CURRENT FILING DATE: 1999-08-05
18 <150> PRIOR APPLICATION NUMBER: 08/834,655
19 <151> PRIOR FILING DATE: 1997-04-11
21 <160> NUMBER OF SEQ ID NOS: 40
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1617
27 <212> TYPE: DNA
28 <213> ORGANISM: Mortierella alpina
30 <220> FEATURE:
31 <223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
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36 tgccgaggct ctgaatgagg gcaagaagga tgccgaggca cccttcttga tgatcatcga 180
37 caacaaggtg tacgatgtcc gcgagttcgt ccctgatcat cccggtggaa gtgtgattct 240
38 cacgcacgtt ggcaaggacg gcactgacgt ctttgacact tttcaccccg aggctgcttg 300
39 ggagactctt gccaactttt acgttggtga tattgacgag agcgaccgcg atatcaagaa 360
40 tgatgacttt gcggccgagg tccgcaagct gcgtaccttg ttccagtctc ttggttacta 420
41 cgattcttcc aaggcatact acgccttcaa ggtctcgttc aacctctgca tctggggttt 480
42 gtcgacggtc attgtggcca agtggggcca gacctcgacc ctcgccaacg tgctctcggc 540
43 tgcgcttttg ggtctgttct ggcagcagtg cggatggttg gctcacgact ttttgcatca 600
44 ccaggtcttc caggaccgtt tctgggggtga tcttttcggc gccttcttgg gaggtgtctg 660
45 ccagggcttc tcgtcctcgt ggtgaagga caagcacaac actcaccacg ccgcccccaa 720
46 cgtccacggc gaggatcccg acattgacac ccaccctctg ttgacctgga gtgagcatgc 780
47 gttggagatg ttctcggatg tcccagatga ggagctgacc cgcatgtagt cgcgtttcat 840
48 ggtcctgaac cagacctggt tttacttccc cattctctcg tttgcccgtc tctcctggtg 900
49 cctccagtcc attctctttg tgctgcctaa cggtcaggcc cacaagccct cgggcgcgcg 960
50 tgtgcccatc tcgttggtcg agcagctgtc gcttgcgatg cactggacct ggtacctcgc 1020
51 caccatgttc ctgttcatca aggatcccgt caacatgctg gtgtacttttt tggtgtcgca 1080
52 ggcggtgtgc ggaaacttgt tggcgatcgt gttctcgctc aaccacaacg gtatgcctgt 1140
53 gatctcgaag gaggaggcgg tcgatatgga tttcttcacg aagcagatca tcacgggtcg 1200
54 tgatgtccac ccgggtctat ttgccaactg gttcacgggt ggattgaact atcagatcga 1260
55 gcaccacttg ttcccttcga tgcctcgcca caacttttca aagatccagc ctgctgtcga 1320
56 gaccctgtgc aaaaagtaca atgtccgata ccacaccacc ggtatgatcg agggaactgc 1380
57 agaggtcttt agccgtctga acgaggtctc caaggctgcc tccaagatgg gtaaggcgca 1440
58 gtaaaaaaaa aaacaaggac gttttttttc gccagtgcct gtgcctgtgc ctgcttccct 1500
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PATENT APPLICATION: US/09/367,013A   TIME: 16:10:58

Input Set : A:\Cgabl.app
Output Set: N:\CRF3\08012000\I367013A.raw

59 tgtcaagtcg agcgtttctg gaaaggatcg ttcagtgcag tatcatcatt ctcctttac 1560
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64 <211> LENGTH: 457
65 <212> TYPE: PRT
66 <213> ORGANISM: Mortierella alpina
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72 Asn Ala Glu Ala Leu Asn Glu Gly Lys Lys Asp Ala Glu Ala Pro Phe
73   20   25   30
75 Leu Met Ile Ile Asp Asn Lys Val Tyr Asp Val Arg Glu Phe Val Pro
76   35   40   45
78 Asp His Pro Gly Gly Ser Val Ile Leu Thr His Val Gly Lys Asp Gly
79   50   55   60
81 Thr Asp Val Phe Asp Thr Phe His Pro Glu Ala Ala Trp Glu Thr Leu
82 65   70   75   80
84 Ala Asn Phe Tyr Val Gly Asp Ile Asp Glu Ser Asp Arg Asp Ile Lys
85   85   90   95
87 Asn Asp Asp Phe Ala Ala Glu Val Arg Lys Leu Arg Thr Leu Phe Gln
88   100   105   110
90 Ser Leu Gly Tyr Tyr Asp Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val
91   115   120   125
93 Ser Phe Asn Leu Cys Ile Trp Gly Leu Ser Thr Val Ile Val Ala Lys
94   130   135   140
96 Trp Gly Gln Thr Ser Thr Leu Ala Asn Val Leu Ser Ala Ala Leu Leu
97 145   150   155   160
99 Gly Leu Phe Trp Gln Gln Cys Gly Trp Leu Ala His Asp Phe Leu His
100   165   170   175
102 His Gln Val Phe Gln Asp Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe
103   180   185   190
105 Leu Gly Gly Val Cys Gln Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys
106   195   200   205
108 His Asn Thr His His Ala Ala Pro Asn Val His Gly Glu Asp Pro Asp
109 210   215   220
111 Ile Asp Thr His Pro Leu Leu Thr Trp Ser Glu His Ala Leu Glu Met
112 225   230   235   240
114 Phe Ser Asp Val Pro Asp Glu Glu Leu Thr Arg Met Trp Ser Arg Phe
115   245   250   255
117 Met Val Leu Asn Gln Thr Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala
118   260   265   270
120 Arg Leu Ser Trp Cys Leu Gln Ser Ile Leu Phe Val Leu Pro Asn Gly
121   275   280   285
123 Gln Ala His Lys Pro Ser Gly Ala Arg Val Pro Ile Ser Leu Val Glu
124   290   295   300
126 Gln Leu Ser Leu Ala Met His Trp Thr Trp Tyr Leu Ala Thr Met Phe
127 305   310   315   320
129 Leu Phe Ile Lys Asp Pro Val Asn Met Leu Val Tyr Phe Leu Val Ser
130   325   330   335

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PATENT APPLICATION: US/09/367,013A   TIME: 16:10:58

Input Set : A:\Cgab1.app
Output Set: N:\CRF3\08012000\I367013A.raw

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135 Asn Gly Met Pro Val Ile Ser Lys Glu Glu Ala Val Asp Met Asp Phe
136           355               360               365
138 Phe Thr Lys Gln Ile Ile Thr Gly Arg Asp Val His Pro Gly Leu Phe
139       370               375               380
141 Ala Asn Trp Phe Thr Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu
142 385               390               395               400
144 Phe Pro Ser Met Pro Arg His Asn Phe Ser Lys Ile Gln Pro Ala Val
145               405               410               415
147 Glu Thr Leu Cys Lys Lys Tyr Asn Val Arg Tyr His Thr Thr Gly Met
148           420               425               430
150 Ile Glu Gly Thr Ala Glu Val Phe Ser Arg Leu Asn Glu Val Ser Lys
151           435               440               445
153 Ala Ala Ser Lys Met Gly Lys Ala Gln
154       450               455
157 <210> SEQ ID NO: 3
158 <211> LENGTH: 1488
159 <212> TYPE: DNA
160 <213> ORGANISM: Mortierella alpina
162 <400> SEQUENCE: 3
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164 ccaccgtctc tcctccaccc tccgagacga ctgcaactgt aatcaggaac cgacaaatac 120
165 acgatttctt tttactcagc accaactcaa aatcctcaac cgcaaccctt tttcaggatg 180
166 gcacctccca acactatcga tgccggtttg acccagcgtc atatcagcac ctcggcccca 240
167 aactcggcca agcctgcctt cgagcgcaac taccagctcc ccgagttcac catcaaggag 300
168 atccgagagt gcatccctgc ccactgcttt gagcgctccg gtctccgtgg tctctgccac 360
169 gttgccatcg atctgacttg ggcgtcgctc ttgttcctgg ctgcgaccca gatcgacaag 420
170 tttgagaatc ccttgatccg ctatttggcc tggcctgttt actggatcat gcagggtatt 480
171 gtctgcaccg gtgtctgggt gctggctcac gagtgtggtc atcagtcctt ctcgacctcc 540
172 aagaccctca acaacacagt tggttggatc ttgcactcga tgctcttggt cccctaccac 600
173 tcctggagaa tctcgcactc gaagcaccac aaggccactg gccatatgac caaggaccag 660
174 gtctttgtgc ccaagacccg ctcccaggtt ggcttgcctc ccaaggagaa cgctgctgct 720
175 gccgttcagg aggaggacat gtccgtgcac ctggatgagg aggctcccat tgtgactttg 780
176 ttctggatgg tgatccagtt cttgttcgga tggcccgcgt acctgattat gaacgcctct 840
177 ggccaagact acggccgctg gacctcgcac ttccacacgt actcgcccat ctttgagccc 900
178 cgcaactttt tcgacattat tatctcggac ctcggtgtgt tggctgccct cggtgccctg 960
179 atctatgcct ccatgcagtt gtcgctcttg accgtcacca agtactatat tgtcccctac 1020
180 ctctttgtca acttttggtt ggtcctgatc accttcttgc agcacaccga tcccaagctg 1080
181 ccccattacc gcgagggtgc ctggaatttc cagcgtggag ctctttgcac cgttgaccgc 1140
182 tcgtttggca agttcttgga ccatatgttc cacggcattg tccacaccca tgtggcccat 1200
183 cacttgttct cgcaaatgcc gttctaccat gctgaggaag ctacctatca tctcaagaaa 1260
184 ctgctgggag agtactatgt gtacgaccca tccccgatcg tcgttgcggt ctggaggtcg 1320
185 ttccgtgagt gccgattcgt ggaggatcag ggagacgtgg tcttttttcaa gaagtaaaaa 1380
186 aaaagacaat ggaccacaca caaccttgtc tctacagacc tacgtatcat gtagccatac 1440
187 cacttcataa aagaacatga gctctagagg cgtgtcattc gcgcctcc       1488
190 <210> SEQ ID NO: 4
191 <211> LENGTH: 399
192 <212> TYPE: PRT
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RAW SEQUENCE LISTING   DATE: 08/01/2000
PATENT APPLICATION: US/09/367,013A   TIME: 16:10:58

Input Set : A:\Cgabl.app
Output Set: N:\CRF3\08012000\I367013A.raw

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195 <400> SEQUENCE: 4
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199 Ser Thr Ser Ala Pro Asn Ser Ala Lys Pro Ala Phe Glu Arg Asn Tyr
200             20                  25                  30
202 Gln Leu Pro Glu Phe Thr Ile Lys Glu Ile Arg Glu Cys Ile Pro Ala
203         35                  40                  45
205 His Cys Phe Glu Arg Ser Gly Leu Arg Gly Leu Cys His Val Ala Ile
206     50                  55                  60
208 Asp Leu Thr Trp Ala Ser Leu Leu Phe Leu Ala Ala Thr Gln Ile Asp
209  65                  70                  75                  80
211 Lys Phe Glu Asn Pro Leu Ile Arg Tyr Leu Ala Trp Pro Val Tyr Trp
212             85                  90                  95
214 Ile Met Gln Gly Ile Val Cys Thr Gly Val Trp Val Leu Ala His Glu
215             100                 105                 110
217 Cys Gly His Gln Ser Phe Ser Thr Ser Lys Thr Leu Asn Asn Thr Val
218     115                 120                 125
220 Gly Trp Ile Leu His Ser Met Leu Leu Val Pro Tyr His Ser Trp Arg
221     130                 135                 140
223 Ile Ser His Ser Lys His His Lys Ala Thr Gly His Met Thr Lys Asp
224 145                 150                 155                 160
226 Gln Val Phe Val Pro Lys Thr Arg Ser Gln Val Gly Leu Pro Pro Lys
227             165                 170                 175
229 Glu Asn Ala Ala Ala Ala Val Gln Glu Glu Asp Met Ser Val His Leu
230             180                 185                 190
232 Asp Glu Glu Ala Pro Ile Val Thr Leu Phe Trp Met Val Ile Gln Phe
233         195                 200                 205
235 Leu Phe Gly Trp Pro Ala Tyr Leu Ile Met Asn Ala Ser Gly Gln Asp
236     210                 215                 220
238 Tyr Gly Arg Trp Thr Ser His Phe His Thr Tyr Ser Pro Ile Phe Glu
239 225                 230                 235                 240
241 Pro Arg Asn Phe Phe Asp Ile Ile Ile Ser Asp Leu Gly Val Leu Ala
242             245                 250                 255
244 Ala Leu Gly Ala Leu Ile Tyr Ala Ser Met Gln Leu Ser Leu Leu Thr
245             260                 265                 270
247 Val Thr Lys Tyr Tyr Ile Val Pro Tyr Leu Phe Val Asn Phe Trp Leu
248         275                 280                 285
250 Val Leu Ile Thr Phe Leu Gln His Thr Asp Pro Lys Leu Pro His Tyr
251     290                 295                 300
253 Arg Glu Gly Ala Trp Asn Phe Gln Arg Gly Ala Leu Cys Thr Val Asp
254 305                 310                 315                 320
256 Arg Ser Phe Gly Lys Phe Leu Asp His Met Phe His Gly Ile Val His
257             325                 330                 335
259 Thr His Val Ala His His Leu Phe Ser Gln Met Pro Phe Tyr His Ala
260     340                 345                 350
262 Glu Glu Ala Thr Tyr His Leu Lys Lys Leu Leu Gly Glu Tyr Tyr Val
263     355                 360                 365
265 Tyr Asp Pro Ser Pro Ile Val Val Ala Val Trp Arg Ser Phe Arg Glu
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RAW SEQUENCE LISTING   DATE: 08/01/2000
PATENT APPLICATION: US/09/367,013A   TIME: 16:10:58

Input Set : A:\Cgabl.app
Output Set: N:\CRF3\08012000\I367013A.raw

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268 Cys Arg Phe Val Glu Asp Gln Gly Asp Val Val Phe Phe Lys Lys
269 385                390                395
272 <210> SEQ ID NO: 5
273 <211> LENGTH: 355
274 <212> TYPE: PRT
275 <213> ORGANISM: Mortierella alpina
277 <400> SEQUENCE: 5
278 Glu Val Arg Lys Leu Arg Thr Leu Phe Gln Ser Leu Gly Tyr Tyr Asp
279  1           5               10              15
281 Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val Ser Phe Asn Leu Cys Ile
282          20              25              30
284 Trp Gly Leu Ser Thr Val Ile Val Ala Lys Trp Gly Gln Thr Ser Thr
285          35              40              45
287 Leu Ala Asn Val Leu Ser Ala Ala Leu Leu Gly Leu Phe Trp Gln Gln
288          50              55              60
290 Cys Gly Trp Leu Ala His Asp Phe Leu His His Gln Val Phe Gln Asp
291  65              70              75              80
293 Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe Leu Gly Gly Val Cys Gln
294          85              90              95
296 Gly Phe Ser Ser Trp Trp Lys Asp Lys His Asn Thr His His Ala
297          100             105             110
299 Ala Pro Asn Val His Gly Glu Asp Pro Asp Ile Asp Thr His Pro Leu
300          115             120             125
302 Leu Thr Trp Ser Glu His Ala Leu Glu Met Phe Ser Asp Val Pro Asp
303          130             135             140
305 Glu Glu Leu Thr Arg Met Trp Ser Arg Phe Met Val Leu Asn Gln Thr
306 145              150             155             160
308 Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala Arg Leu Ser Trp Cys Leu
309          165             170             175
311 Gln Ser Ile Leu Phe Val Leu Pro Asn Gly Gln Ala His Lys Pro Ser
312          180             185             190
314 Gly Ala Arg Val Pro Ile Ser Leu Val Glu Gln Leu Ser Leu Ala Met
315          195             200             205
317 His Trp Thr Trp Tyr Leu Ala Thr Met Phe Leu Phe Ile Lys Asp Pro
318          210             215             220
320 Val Asn Met Leu Val Tyr Phe Leu Val Ser Gln Ala Val Cys Gly Asn
321 225              230             235             240
323 Leu Leu Ala Ile Val Phe Ser Leu Asn His Asn Gly Met Pro Val Ile
324          245             250             255
326 Ser Lys Glu Glu Ala Val Asp Met Asp Phe Phe Thr Lys Gln Ile Ile
327          260             265             270
329 Thr Gly Arg Asp Val His Pro Gly Leu Phe Ala Asn Trp Phe Thr Gly
330          275             280             285
332 Gly Leu Asn Tyr Gln Ile Glu His His Leu Phe Pro Ser Met Pro Arg
333          290             295             300
335 His Asn Phe Ser Lys Ile Gln Pro Ala Val Glu Thr Leu Cys Lys Lys
336 305              310             315             320
338 Tyr Asn Val Arg Tyr His Thr Thr Gly Met Ile Glu Gly Thr Ala Glu
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Please Note:
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.**

VERIFICATION SUMMARY   DATE: 08/01/2000
PATENT APPLICATION: US/09/367,013A   TIME: 16:10:59

Input Set : A:\Cgabl.app
Output Set: N:\CRF3\08012000\I367013A.raw

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L:360 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:360 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:363 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:363 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
M:340 Repeated in SeqNo=6
L:366 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:366 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:444 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:444 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:444 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
L:447 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:447 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
M:340 Repeated in SeqNo=8
L:465 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:465 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:493 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9
L:493 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
L:493 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:493 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:493 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
L:558 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
L:558 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:558 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
L:726 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20
L:726 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20
L:726 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:20
L:736 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:21
L:736 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:736 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:736 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:21
L:736 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:21
L:743 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:21
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L:743 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:21
M:340 Repeated in SeqNo=21
L:744 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:21
L:744 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
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L:744 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:21
L:757 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:22
L:757 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:757 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:22
L:760 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:22
L:760 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
M:340 Repeated in SeqNo=22
L:1173 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
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VERIFICATION SUMMARY   DATE: 08/01/2000
PATENT APPLICATION: US/09/367,013A   TIME: 16:10:59

Input Set : A:\Cgabl.app
Output Set: N:\CRF3\08012000\I367013A.raw

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L:1173 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
L:1173 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:34
L:1176 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
L:1176 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
M:340 Repeated in SeqNo=34
L:1182 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
L:1182 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
L:1185 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
L:1185 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
L:1232 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:35
L:1232 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:35
L:1232 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:35
L:1235 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:35
L:1235 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:35
M:340 Repeated in SeqNo=35
L:1238 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:35
L:1238 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:35
L:1272 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:36
L:1330 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:37
L:1401 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:38
M:340 Repeated in SeqNo=38
L:1529 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:39
M:340 Repeated in SeqNo=39
L:1684 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:40
M:340 Repeated in SeqNo=40
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